

SEQUENCE LISTING

<110> Gurney, Mark E.
Li, Jinhe
Pauley, Adele M.
Pharmacia & Upjohn Company

<120> Human Sel-10 Polypeptides and Polynucleotides that
Encode Them

<130> 6142

<140> 6142

<141> 1997-12-19

<160> 27

<170> PatentIn Ver. 2.0

<210> 1

<211> 3550

<212> DNA

<213> Homo sapiens

<400> 1

ctcattattc cctcgagttc ttctcagtc a gctgcatgt atgtatgtgt gtcccagaaa 60
gcggtttgat actgagctgc atttgcttt actgtggagt ttgttgccg gttctgctcc 120
ctaactctcc ttttctgacg tgctgagca tgtccacatt agaactctgtg acatacctac 180
ctgaaaaagg tttatattgt cagagactgc caagcagccg gacacacggg ggcacagaat 240
cactgaagg gaaaaataca gaaaataagg gtttctacgg cacattaata atgatttttt 300
acaaaatgaa aagaaagttg gaccatggtt ctgaggtccg ctctttttct ttgggaaaga 360
aaccatgcaa agtctcagaa tatacaagta ccaactgggt tgtaccatgt tcagcaaacac 420
caacaacttt tggggacctc agagcagcca atggccaagg gcaacaacga cgccgaatta 480
catctgtcca gccacctaca ggcctccagg aatggctaaa aatgtttcag agctggagtg 540
gaccagagaa attgcttgct ttagatgaac tcattgatag ttgtgaacca acacaagtaa 600
aacatatgat gcaagtgata gaacccagc ttcaacgaga cttcatttca ttgctccta 660

*Sub
a1*

5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
105
110
115
120
125
130
135
140
145
150
155
160
165
170
175
180
185
190
195
200
205
210
215
220
225
230
235
240
245
250
255
260
265
270

aagagttggc actctatgtg ctttcattcc tggaaaccaa agacctgcta caagcagctc 720
 agacatgtcg ctactggaga attttggctg aagacaacct tctctggaga gagaaatgca 780
 aagaagaggg gattgatgaa ccattgcaca tcaagagaag aaaagtaata aaaccaggtt 840
 tcatacacag tccatggaaa agtgcataca tcagacagca cagaattgat actaactgga 900
 ggcgaggaga actcaaatct cctaaggctc tgaaggaca tgatgatcat gtgatcacat 960
 gcttacagtt ttgtggtaac cgaatagtta gtggttctga tgacaacact ttaaaagttt 1020
 ggtcagcagt cacaggcaaa tgtctgagaa cattagtggg acatacagggt ggagtatggt 1080
 catcacaat gagagacaac atcatcata gtggatctac agatcggaca ctcaaagtgt 1140
 ggaatgcaga gactggagaa tgtatacada ccttatatgg gcatacttcc actgtgcggt 1200
 gtatgcatct tcatgaaaaa agagttgtta gcggttctcg agatgccact cttagggttt 1260
 gggatattga gacagggcag tgtttcatg tttttagtggg tcatgttgca gcagtccgct 1320
 gtgttcaata tgatggcagg agggttgtta gtggagcata tgattttatg gtaaagggtgt 1380
 gggatccaga gactgaaacc tgtctacaca cgttgcaggg gcatactaata agagtctatt 1440
 cattacagtt tgatgggtatc catgtgggtga gtggatctct tgatacatca atccgtgttt 1500
 gggatgtgga gacaggggat tgcattcaca cgttacagg gcaccagtcg ttaacaagtgt 1560
 gaatggaact caaagacaat attcttgtct ctgggaatgc agattctaca gttaaaatct 1620
 gggatatcaa aacaggacag tgtttacaaa cattgcaagg tccaacaag catcagagtgt 1680
 ctgtgacctg ttacagttc aacaagaact ttgttaattac cagctcagat gatggaactgt 1740
 taaaactatg ggacttgaaa acgggtgaaat ttattcgaaa cctagtcaca ttggagagtgt 1800
 gggggagtgg gggagttgtg tggcggatca gagcctcaaa cacaagctg gtgtgtgcag 1860
 ttgggagtcg gaatgggact gaagaaacca agctgtctgggt gctggacttt gatgtggaca 1920
 tgaagtgaag agcagaaaag atgaatttgt ccaattgtgt agacgatata ctccctgcc 1980
 tccccctgc aaaaagaaaa aaagaaaga aaaagaaaa aatccttgt tctcagtgg 2040
 gcaggatgtt ggcttggggc aacagattga aaagacctac agactaagaa ggaaaagaag 2100
 aagagatgac aaaccataac tgacaagaga ggcgtctgct gtctcatcac ataaaaggct 2160
 tcaactttga ctgagggcag ctttgcaaaa tgagacttcc taaatcaaac caggtgcaat 2220
 tatttctta ttttctctc cagtggctcat tggggcagtg ttaatgctga aacatcatta 2280
 cagattctgc tagcctgttc ttttaccact gacagctaga cacctagaaa ggaactgcaa 2340
 taatatcaaa acaagtactg gttgacttcc taattagaga gcactctgcaa caaaaagtca 2400
 tttttctgga gtggaaaagc ttaaaaaaat tactgtgaa ttgttttgta cagttatcat 2460
 gaaaagcttt ttttttatt tttngccaa ccattgccaa tgtcaatcaa tcacagtatt 2520
 agcctctggt aatctattha ctgttgcttc catatacatt ctcaatgca tatgttctgc 2580
 aaagggtgca agttgtcctg ggttctgtga gtccctgagat ggatttaatt cttgatgctg 2640
 gtgctagaag taggtcttca aatatgggat tgttgcctca acctgtact gtactcccag 2700

6655726666

tggccaaact tatttatgct gctaaatgaa agaaagaaaa aagcaaatta tttttttat 2760
ttttttctg ctgtgacggt ttagtcccag actgaattcc aaatttgctc tagtttggtt 2820
atggaaaaaa gactttttgc cactgaaact tgagccatct gtgcctctaa gaggctgaga 2880
atggaagagt ttcagataat aaagagtga gtttgctgc aagtaaagaa ttgagagtgt 2940
gtgcaaagct tattttcttt tatctgggca aaaattaaaa cacattcctt ggaacagagc 3000
tattacttgc ctgttctgtg gagaaacttt tctttttgag ggctgtggtg aatggatgaa 3060
cgtacatcgt aaaactgaca aaatatttta aaaatatata aaacacaaaa ttaaaataaa 3120
gttgctggtc agtcttagtg ttttacagta tttgggaaaa caactgttac agttttattg 3180
ctctgagtaa ctgacaaagc agaaactatt cagtttttgt agtaaaggcg tcacatgcaa 3240
acaaacaaaa tgaatgaaac agtcaaatgg tttgcctcat tctccaagag ccacaactca 3300
agctgaaactg tgaagtggt ttaacactgt atcctaggcg atcttttttc ctccttctgt 3360
ttattttttt gnttgtttta tttatagctt gatttaaaac aatcagattc aagttggtta 3420
attttagtta tgtaacaacc tgacatgatg gaggaaaaca acctttaaag ggattgtgtc 3480
tatggtttga ttcacttaga aattttattt tcttataact taagtgcaat aaaatgtggt 3540
ttttcatgtt 3550

<210> 2

<211> 3571

<212> DNA

<213> Homo sapiens

<400> 2

ctcagcaggt caggacattt ggtaggggaa ggttgaaga caaaagcagc aggccttggg 60
ttctcagcct tttaaaaact attattaaat atatattttt aaaatttagt ggtagagct 120
tttagtaatg tgctgtatt acatgtagag agtattcgtc aaccaagagg agttttaaaa 180
tgtcaaaacc gggaaaacct actctaaacc atggcttggg tctgttgat cttaaaagtg 240
caaaagagcc tctaccacat caaacctga tgaagatatt tagcattagc atcattgccc 300
aaggcctccc tttttgtcga agacggatga aaagaaagtt ggaccatggt tctgagggtc 360
gctctttttc tttgggaaag aaaccatgca aagtctcaga atatacaagt accactgggc 420
ttgtaccatg ttcagcaaca ccaacaactt ttggggacct cagagcagcc aatggccaag 480
ggcaacaacg acgccgaatt acatctgtcc agccacctac aggcctccag gaatggctaa 540
aatgtttca gagctggagt ggaccagaga aattgcttgc tttagatgaa ctattgata 600
gttgatgacc aacacaagta aaacatatga tgcaagtgat agaaccagcag tttcaacgag 660
acttcatttc attgctccct aaagagttgg cactctatgt gcttttattc ctggaacca 720
aagacctgct acaagcagct cagacatgct gctactggag aattttgct gaagacaacc 780

ttctctggag agagaaatgc aaagaagagg ggattgatga accattgcac atcaagagaa 840
 gaaaagtaat aaaaccaggt ttcatacaca gtccatggaa aagtgcatac atcagacagc 900
 acagaattga tactaactgg aggcgaggag aactcaaate tctaagggtg ctgaaaggac 960
 atgatgatca tgtgatcaca tgcttacagt tttgtggtaa ccgaatagtt agtggttctg 1020
 atgacaacac tttaaaagt tggtcagcag tcacaggcaa atgtctgaga acattagtgg 1080
 gacatacagg tggagtatgg tcatcacaaa tgagagacaa catcatcatt agtggatcta 1140
 cagatcggac actcaaagt tggaatgcag agactggaga atgtatacac acctatatg 1200
 ggcatacttc cactgtgcgt tgtatgcatc ttcatgaaaa aagagttggt agcggttctc 1260
 gagatgccac tcttagggtt tgggatattg agacaggcca gtgtttacat gttttgatgg 1320
 gtcatgttgc agcagtcgc tgtgttcaat atgatggcag gagggttggt agtggagcat 1380
 atgattttat ggtaaagggt tgggatccag agactgaaac ctgtctacac acgttgcagg 1440
 ggcatactaa tagagtctat tcattacagt ttgatgggat ccatgtgggt agtggatctc 1500
 ttgatacatc aatccgtggt tgggatgtgg agacaggaa ttgcattcac acgttaacag 1560
 ggcaccagtc gttaacaagt ggaatggaac tcaaagacaa tattcttgtc tctgggaatg 1620
 cagattctac agttaaaatc tgggatatca aacaggaca gtgtttacaa acattgcaag 1680
 gtccaacaa gcatacagagt gctgtgacct gtttacagtt caacaagaac tttgtaatta 1740
 ccagctcaga tgatggaact gtaaaactat gggacttgaa aacgggtgaa tttattcgaa 1800
 acctagtcac attggagagt ggggggagtg ggggagttgt gtggcggatc agagcctcaa 1860
 acacaaagct ggtgtgtgca gttgggagtc gyaatgggac tgaagaaacc aagctgctgg 1920
 tgctggactt tgatgtggac atgaagtga gagcagaaaa gatgaatttg tccaattgtg 1980
 tagacgatat actccctgcc cttccccctg caaaaagaaa aaaagaaaag aaaaagaaaa 2040
 aaatcccttg ttctcagtg tgcaggatgt tggcttgggg caacagattg aaaagaccta 2100
 cagactaaga aggaaaagaa gaagagatga caaacataa ctgacaagag aggcgtctgc 2160
 tgtctcatca cataaaaggc ttcacttttg actgagggca gctttgcaaa atgagacttt 2220
 ctaaatacaa ccaggtgcaa ttatttcttt attttcttct ccagtggtea ttggggcagt 2280
 gttaatgctg aaacatcatt acagattctg ctagcctggt cttttaccac tgacagctag 2340
 acacctagaa aggaactgca ataatatcaa aacaagtact ggttgacttt ctaattagag 2400
 agcatctgca acaaaaagtc attttcttg agtggaaaag cttaaaaaaa ttactgtgaa 2460
 ttgtttttgt acagttatca tgaagaagct tttttttat tttttngcca accattgcc 2520
 atgtcaatca atcacagtat tagcctctgt taatctattt actggtgctt ccatatacat 2580
 tcttcaatgc atatgttgc caaagggtgc aagttgtcct gggttctgtg agtctgaga 2640
 tggatttaat tcttgatgct ggtgctagaa gtaggtcttc aaatatggga ttgttgtccc 2700
 aaccctgtac tgtactccca gtggccaaac ttatttatgc tgctaaatga aagaaagaaa 2760
 aaagcaaatt atttttttta tttttttct gctgtgacgt tttagtccca gactgaattc 2820

66650:2288-3571

caaatttgct ctagtttggt tatggaaaa agactttttg cactgaaac ttgagccatc 2880
 tgtgcctcta agaggctgag aatggaagag tttcagataa taaagagtga agtttgctg 2940
 caagtaaaga attgagagtg tgtgcaaagc ttattttctt ttatctgggc aaaaattaaa 3000
 acacattcct tggaacagag ctattacttg cctgttctgt ggagaaactt ttctttttga 3060
 gggctgtggt gaatggatga acgtacatcg taaaactgac aaaatatttt aaaaatatat 3120
 aaaacacaaa attaaaataa agttgctggt cagtcttagt gttttacagt atttgggaaa 3180
 acaactgtta cagttttatt gctctgagta actgacaaaag cagaaactat tcagtttttg 3240
 tagtaaaggc gtcacatgca aacaaacaaa atgaatgaaa cagtcaaatg gtttgctca 3300
 ttctccaaga gccacaactc aagctgaact gtgaaagtgg ttttaactg tctcttaggc 3360
 gatctttttt cctccttctg tttatttttt tgnttgtttt atttatagtc tgatttaaaa 3420
 caatcagatt caagttgggt aattttagtt atgtaacaac ctgacatgat ggaggaaaac 3480
 aacctttaa gggattgtgt ctatggtttg attcacttag aaattttatt ttcttataac 3540
 ttaagtcaa taaaatgtgt ttttcatgt t 3571

<210> 3

<211> 627

<212> PRT

<213> Homo sapiens

<400> 3

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr
 1 5 10 15
 Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr
 20 25 30
 Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys
 35 40 45
 Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr
 50 55 60
 Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr
 65 70 75 80

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser
85 90 95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu
100 105 110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr
115 120 125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg
130 135 140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met
145 150 155 160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu
165 170 175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile
180 185 190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu
195 200 205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala
210 215 220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu
225 230 235 240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile
245 250 255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys

260

265

270

Ser	Ala	Tyr	Ile	Arg	Gln	His	Arg	Ile	Asp	Thr	Asn	Trp	Arg	Arg	Gly
		275					280					285			

Glu	Leu	Lys	Ser	Pro	Lys	Val	Leu	Lys	Gly	His	Asp	Asp	His	Val	Ile
		290				295						300			

Thr	Cys	Leu	Gln	Phe	Cys	Gly	Asn	Arg	Ile	Val	Ser	Gly	Ser	Asp	Asp
305					310					315					320

Asn	Thr	Leu	Lys	Val	Trp	Ser	Ala	Val	Thr	Gly	Lys	Cys	Leu	Arg	Thr
				325					330					335	

Leu	Val	Gly	His	Thr	Gly	Gly	Val	Trp	Ser	Ser	Gln	Met	Arg	Asp	Asn
		340						345						350	

Ile	Ile	Ile	Ser	Gly	Ser	Thr	Asp	Arg	Thr	Leu	Lys	Val	Trp	Asn	Ala
		355					360						365		

Glu	Thr	Gly	Glu	Cys	Ile	His	Thr	Leu	Tyr	Gly	His	Thr	Ser	Thr	Val
		370				375						380			

Arg	Cys	Met	His	Leu	His	Glu	Lys	Arg	Val	Val	Ser	Gly	Ser	Arg	Asp
385					390						395				400

Ala	Thr	Leu	Arg	Val	Trp	Asp	Ile	Glu	Thr	Gly	Gln	Cys	Leu	His	Val
				405					410						415

Leu	Met	Gly	His	Val	Ala	Ala	Val	Arg	Cys	Val	Gln	Tyr	Asp	Gly	Arg
		420						425						430	

Arg	Val	Val	Ser	Gly	Ala	Tyr	Asp	Phe	Met	Val	Lys	Val	Trp	Asp	Pro
		435					440							445	

2025 RELEASE

625

<210> 4

<211> 592

<212> PRT

<213> Homo sapiens

<400> 4

Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys Gly Leu Tyr
1 5 10 15

Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr Glu Ser Leu
20 25 30

Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr Leu Lys Met
35 40 45

Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg
50 55 60

Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser
65 70 75 80

Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp
85 90 95

Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser
100 105 110

Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser
115 120 125

Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser
130 135 140

Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln
145 150 155 160

Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr
165 170 175

Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr
180 185 190

Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu
195 200 205

Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg
210 215 220

Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr
225 230 235 240

Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys
245 250 255

Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu
260 265 270

Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu
275 280 285

Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly
290 295 300

His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile
305 310 315 320

000000000000000000

Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly
 325 330 335
 Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met
 340 345 350
 His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu
 355 360 365
 Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly
 370 375 380
 His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val
 385 390 395 400
 Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu
 405 410 415
 Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu
 420 425 430
 Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile
 435 440 445
 Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly
 450 455 460
 His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val
 465 470 475 480
 Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly
 485 490 495
 Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val
 500 505 510

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

000000000000000000

Thr Cys Leu Glu Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp
515 520 525

Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn
530 535 540

Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile
545 550 555 560

Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly
565 570 575

Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
580 585 590

<210> 5

<211> 553

<212> PRT

<213> Homo sapiens

<400> 5

Met Gly Phe Tyr Gly Thr Leu Lys Met Ile Phe Tyr Lys Met Lys Arg
1 5 10 15

Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu Gly Lys Lys
20 25 30

Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys
35 40 45

000000000000

Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln
50 55 60

Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro Thr Gly Leu
65 70 75 80

Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu
85 90 95

Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr Gln Val Lys
100 105 110

His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser
115 120 125

Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro
130 135 140

Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu
145 150 155 160

Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile
165 170 175

Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys Pro Gly Phe
180 185 190

Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His Arg Ile Asp
195 200 205

Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val Leu Lys Gly
210 215 220

His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile

225 230 235 240

Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser Ala Val Thr
245 250 255

Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly Val Trp Ser
260 265 270

Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr
275 280 285

Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His Thr Leu Tyr
290 295 300

Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu Lys Arg Val
305 310 315 320

Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp Ile Glu Thr
325 330 335

Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala Val Arg Cys
340 345 350

Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr Asp Phe Met
355 360 365

Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His Thr Leu Gln
370 375 380

Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly Ile His Val
385 390 395 400

Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp Val Glu Thr
405 410 415

0123456789

66050-2283E60

Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu Thr Ser Gly
420 425 430

Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala Asp Ser Thr
435 440 445

Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln
450 455 460

Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln Phe Asn Lys
465 470 475 480

Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys Leu Trp Asp
485 490 495

Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu Glu Ser Gly
500 505 510

Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu
515 520 525

Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu
530 535 540

Val Leu Asp Phe Asp Val Asp Met Lys
545 550

<210> 6

<211> 545

<212> PRT

<213> Homo sapiens

<400> 6

16010000200000

Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val
 1 5 10 15
 Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr
 20 25 30
 Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly
 35 40 45
 Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr
 50 55 60
 Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln
 65 70 75 80
 Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp
 85 90 95
 Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro
 100 105 110
 Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu
 115 120 125
 Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln
 130 135 140
 Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg
 145 150 155 160
 Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg
 165 170 175
 Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala

Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser
370 375 380

Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser
385 390 395 400

Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr
405 410 415

Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu
420 425 430

Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr
435 440 445

Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala
450 455 460

Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp
465 470 475 480

Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg
485 490 495

Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg
500 505 510

Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn
515 520 525

Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met
530 535 540

Lys

545

<210> 7

<211> 540

<212> PRT

<213> Homo sapiens

<400> 7

Met	Lys	Arg	Lys	Leu	Asp	His	Gly	Ser	Glu	Val	Arg	Ser	Phe	Ser	Leu
1				5					10					15	

Gly	Lys	Lys	Pro	Cys	Lys	Val	Ser	Glu	Tyr	Thr	Ser	Thr	Thr	Gly	Leu
			20					25						30	

Val	Pro	Cys	Ser	Ala	Thr	Pro	Thr	Thr	Phe	Gly	Asp	Leu	Arg	Ala	Ala
		35					40					45			

Asn	Gly	Gln	Gly	Gln	Gln	Arg	Arg	Arg	Ile	Thr	Ser	Val	Gln	Pro	Pro
	50						55					60			

Thr	Gly	Leu	Gln	Glu	Trp	Leu	Lys	Met	Phe	Gln	Ser	Trp	Ser	Gly	Pro
65					70					75				80	

Glu	Lys	Leu	Leu	Ala	Leu	Asp	Glu	Leu	Ile	Asp	Ser	Cys	Glu	Pro	Thr
				85					90					95	

Gln	Val	Lys	His	Met	Met	Gln	Val	Ile	Glu	Pro	Gln	Phe	Gln	Arg	Asp
				100					105					110	

Phe	Ile	Ser	Leu	Leu	Pro	Lys	Glu	Leu	Ala	Leu	Tyr	Val	Leu	Ser	Phe
		115						120					125		

Leu	Glu	Pro	Lys	Asp	Leu	Leu	Gln	Ala	Ala	Gln	Thr	Cys	Arg	Tyr	Trp
130							135				140				

00000000000000000000

00000000000

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu
145 150 155 160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys
165 170 175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His
180 185 190

Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val
195 200 205

Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly
210 215 220

Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser
225 230 235 240

Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly
245 250 255

Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr
260 265 270

Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His
275 280 285

Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu
290 295 300

Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp
305 310 315 320

166550-266660

Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala
325 330 335

Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr
340 345 350

Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His
355 360 365

Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly
370 375 380

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp
385 390 395 400

Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu
405 410 415

Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala
420 425 430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln
435 440 445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln
450 455 460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys
465 470 475 480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu
485 490 495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn
500 505 510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr
 515 520 525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
 530 535 540

<210> 8

<211> 589

<212> PRT

<213> Homo sapiens

<400> 8

Met Ser Lys Pro Gly Lys Pro Thr Leu Asn His Gly Leu Val Pro Val
 1 5 10 15

Asp Leu Lys Ser Ala Lys Glu Pro Leu Pro His Gln Thr Val Met Lys
 20 25 30

Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys Arg Arg
 35 40 45

Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser
 50 55 60

Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly
 65 70 75 80

Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala
 85 90 95

Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro
 100 105 110

Sequences: 210-213

"A32020"

290	295	300	
Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser			
305	310	315	320
Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile			
	325	330	335
His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His			
	340	345	350
Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp			
	355	360	365
Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala			
370	375	380	
Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala			
385	390	395	400
Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu			
	405	410	415
His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp			
	420	425	430
Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp			
	435	440	445
Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser			
450	455	460	
Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn			
465	470	475	480

Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu
485 490 495

Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu
500 505 510

Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val
515 520 525

Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr
530 535 540

Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser
545 550 555 560

Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu
565 570 575

Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
580 585

<210> 9

<211> 559

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys
1 5 10 15

Arg Arg Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser
20 25 30

000030 = 222222

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300

Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr
35 40 45
Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu
50 55 60
Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val
65 70 75 80
Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp
85 90 95
Ser Gly Pro Glu Lys Leu Leu Ala Ile Asp Glu Leu Ile Asp Ser Cys
100 105 110
Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe
115 120 125
Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val
130 135 140
Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys
145 150 155 160
Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys
165 170 175
Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys
180 185 190
Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile
195 200 205
Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser

00000000000000000000

210	215	220															
Pro	Lys	Val	Leu	Lys	Gly	His	Asp	Asp	His	Val	Ile	Thr	Cys	Leu	Gln		
225					230						235				240		
Phe	Cys	Gly	Asn	Arg	Ile	Val	Ser	Gly	Ser	Asp	Asp	Asn	Thr	Leu	Lys		
				245						250					255		
Val	Trp	Ser	Ala	Val	Thr	Gly	Lys	Cys	Leu	Arg	Thr	Leu	Val	Gly	His		
			260						265					270			
Thr	Gly	Gly	Val	Trp	Ser	Ser	Gln	Met	Arg	Asp	Asn	Ile	Ile	Ile	Ser		
			275				280							285			
Gly	Ser	Thr	Asp	Arg	Thr	Leu	Lys	Val	Trp	Asn	Ala	Glu	Thr	Gly	Glu		
	290						295					300					
Cys	Ile	His	Thr	Leu	Tyr	Gly	His	Thr	Ser	Thr	Val	Arg	Cys	Met	His		
305							310					315			320		
Leu	His	Glu	Lys	Arg	Val	Val	Ser	Gly	Ser	Arg	Asp	Ala	Thr	Leu	Arg		
							325					330			335		
Val	Trp	Asp	Ile	Glu	Thr	Gly	Gln	Cys	Leu	His	Val	Leu	Met	Gly	His		
				340							345				350		
Val	Ala	Ala	Val	Arg	Cys	Val	Gln	Tyr	Asp	Gly	Arg	Arg	Val	Val	Ser		
			355												365		
Gly	Ala	Tyr	Asp	Phe	Met	Val	Lys	Val	Trp	Asp	Pro	Glu	Thr	Glu	Thr		
			370												380		
Cys	Leu	His	Thr	Leu	Gln	Gly	His	Thr	Asn	Arg	Val	Tyr	Ser	Leu	Gln		
385							390								395		400

<213> Homo sapiens

<400> 10

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu
 1 5 10 15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu
 20 25 30

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala
 35 40 45

Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro
 50 55 60

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro
 65 70 75 80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr
 85 90 95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp
 100 105 110

Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe
 115 120 125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp
 130 135 140

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu
 145 150 155 160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys
 165 170 175

000

0000000000000000

Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His
355 360 365

Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly
370 375 380

Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp
385 390 395 400

Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu
405 410 415

Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala
420 425 430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln
435 440 445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln
450 455 460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys
465 470 475 480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu
485 490 495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn
500 505 510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr
515 520 525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys
530 535 540

SEQUENCE

<210> 11

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 11

cgggatccac catggatgat ggatcgatga cacc

34

<210> 12

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 12

ggaattcctt aagggtatac agcatcaaag tcg

33

<210> 13

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

<400> 13

tcacttcacg tccacatcaa agtcc

25

<210> 14

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 14

ggtaattaca agttcttggt gaactg

26

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 15

ccctgcaacg tgtgtagaca gg

22

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 16

ccagtctctg cattccacac ttg

24

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 17

ctcagacagg tcaggacatt tgg

23

<210> 18

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 18

ggaattccat gaaaagattg gaccatggtt ctg

33

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 19

ggaattcctc acttcatgtc acatcaaagt ccag

34

<210> 20

<211> 1881

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged

homo sapiens

<400> 20

atggagcaaa agctcatttc tgaagaggac ttgaatgaaa tggagcaaaa gctcatttct 60
gaagaggact tgaatgaaat ggagcaaaag ctcatctctg aagaggactt gaatgaaatg 120
gagcaaaagc tcatttctga agaggacttg aatgaaatgg agcaaaagct catttctgaa 180
gaggacttga atgaaatgga gagcttgggc gacctacca tggagcaaaa gctcatttct 240
gaagaggact tgaattccat gaaaagaag ttggaccatg gttctgaggt ccgctctttt 300
tctttgggaa agaaaccatg caaagtctca gaatatacaa gtaccactgg gcttgtagca 360
tgttcagcaa caccaacaac ttttggggac ctgagagcag ccaatggcca agggcaacaa 420
cgagccgaa ttacatctgt ccagccacct acaggcctcc aggaatggct aaaaatgttt 480
cagagctgga gtggaccaga gaaattgctt gctttagatg aactcattga tagttgtgaa 540
ccaacacaag taaaacatat gatgcaagtg atagaacccc agtttcaacg agacttcatt 600
tcattgctcc ctaaagagtt ggcactctat gtgctttcat tcttgggaacc caaagacctg 660
ctacaagcag ctgagacatg tgctactgg agaattttgg ctgaagacaa ccttctctgg 720
agagagaaat gcaagaaga ggggattgat gaacattgc acatcaagag aagaaaagta 780
ataaaaccag gtttcataca cagtccatgg aaaagtgcac acatcagaca gcacagaatt 840
gatactaact ggaggcgagg agaactcaaa tctcctaagg tgctgaaagg acatgatgat 900
catgtgatca catgcttaca gttttgtggt aaccgaatag ttagtggttc tgatgacaac 960
actttaaag tttggtcagc agtcacaggc aatgtctga gaacattagt gggacataca 1020
ggtggagtat ggtcatcaca aatgagggac aacatcatca ttagtggatc tacagatcgg 1080

acactcaaag tgtggaatgc agagactgga gaatgtatac acaccttata tgggcatact 1140
tccactgtgc gttggtatgca tcttcatgaa aaaagagttg ttagcgggtc tcgagatgcc 1200
actcttaggg tttgggatat tgagacaggc cagtgtttac atgttttgat gggcatggtt 1260
gcagcagtc cgtgtgttca atatgatggc aggagggttg ttagtggagc atatgatttt 1320
atggtaaagg tgtgggatcc agagactgaa acctgtctac acacgttgca ggggcatact 1380
aatagagtct attcattaca gtttgatggt atccatgtgg tgagtggatc tcttgataca 1440
tccatccgtg tttgggatgt ggagacaggg aattgcattc acacgttaac agggcaccag 1500
tcgttaacaa gtggaatgga actcaaagac aatattcttg tctctgggaa tgcagattct 1560
acagttaaaa tctgggatat caaacagga cagtgtttac aaacattgca aggtcccaac 1620
aagcatcaga gtgctgtgac ctgtttacag ttcaacaaga actttgtaat taccagctca 1680
gatgatggaa ctgtaaaact atgggacttg aaaacgggtg aatttattcg aaacctagtc 1740
acattggaga gtgggggggag tgggggagtt gtgtggcgga tcagagcctc aaacacaaag 1800
ctgggtgtgtg cagtggggag tgggaatggg actgaagaaa ccaagctgct ggtgctggac 1860
tttgatgtgg acatgaagtg a 1881

6666666666666666

<210> 21

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged
homo sapien

<400> 21

Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln
1 5 10 15
Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile
20 25 30
Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu
35 40 45

Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys
245 250 255

Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser
260 265 270

Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu
275 280 285

Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr
290 295 300

Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn
305 310 315 320

Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu
325 330 335

Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile
340 345 350

Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu
355 360 365

Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg
370 375 380

Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala
385 390 395 400

Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu
405 410 415

Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg
420 425 430

Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu
435 440 445

Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr
450 455 460

Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr
465 470 475 480

Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu
485 490 495

Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile
500 505 510

Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys
515 520 525

Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser
530 535 540

Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser
545 550 555 560

Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile
565 570 575

Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp
580 585 590

Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg
595 600 605

Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp
610 615 620

Met Lys
625

<210> 22

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 22

gggtaccctt cattattccc tcgagtttt c

31

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 23

ggaattcctt catgtccaca tcaaagtcc

29

<210> 24

<211> 2010

000000000000

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged
homo sapien

<400> 24

atgtgtgtcc cgagaagcgg ttgatactg agctgcattt gcctttactg tggagttttg 60
ttgccggttc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120
tctgtgacat acctacctga aaaaggttta tattgtcaga gactgccaaag cagccggaca 180
cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240
ttaaaaatga ttttttacia aatgaaaaga aagttggacc atggttctga ggtccgctct 300
ttttctttgg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360
ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420
caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480
tttcagagct ggagtggacc agagaaattg cttgctttag atgaactcat tgatagttgt 540
gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600
atctcattgc tcctaaaga gttggcactc tatgtgcttt cattctgga acccaaagac 660
ctgtacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720
tggagagaga aatgcaaaga agaggggatt gatgaacat tgcacatcaa gagaagaaaa 780
gtaataaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840
attgatacta actggaggcg aggagaaactc aaatctccta aggtgctgaa aggacatgat 900
gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960
aacactttaa aagtttggtc agcagtcaca ggcaaattgc tgagaacatt agtgggacat 1020
acaggtggag tatggtcac acaaatgaga gacaacatca tcattagtgg atctacagat 1080
cggacactca aagtgtggaa tgcagagact ggagaatgta tacacacctt atatgggcat 1140
acttccactg tgcgttgtat gcatcttcat gaaaaaagag ttgttagcgg ttctcgagat 1200
gccacttta gggtttggga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260
gttcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320
tttatggtaa aggtgtggga tccagagact gaaacctgtc tacacacggt gcaggggcat 1380
actaatagag tctattcatt acagtttgat ggtatccatg tggtagtgg atctcttgat 1440
acatcaatcc gtgtttggga tgtggagaca gggaaattgca ttcacacggt aacagggcac 1500
cagtcgttaa caagtggaat ggaactcaaa gacaatattc ttgtctctgg gaatgcagat 1560
tctacagtta aaatctggga tatcaaaaca ggacagtgtt tacaacatt gcaagggtccc 1620

aacaagcadc agagtgctgt gacctgttta cagttcaaca agaactttgt aattaccagc 1680
 tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740
 gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800
 aagctgggtgt gtgcagttgg gactcgggaat gggactgaag aaaccaagct gctggtgctg 1860
 gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920
 tctagagggc ccttcgaagg taagcctatc cctaaccctc tctctgggtct cgattctacg 1980
 cgtaccggtc atcatcacca tcaccattga 2010

<210> 25

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged

homo sapien

<400> 25

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr
 1 5 10 15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr
 20 25 30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys
 35 40 45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr
 50 55 60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr
 65 70 75 80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

GENE: 262626

160155145135125115105100

					85						90						95
Glu	Val	Arg	Ser	Phe	Ser	Leu	Gly	Lys	Lys	Pro	Cys	Lys	Val	Ser	Glu		
					100				105						110		
Tyr	Thr	Ser	Thr	Thr	Gly	Leu	Val	Pro	Cys	Ser	Ala	Thr	Pro	Thr	Thr		
					115				120						125		
Phe	Gly	Asp	Leu	Arg	Ala	Ala	Asn	Gly	Gln	Gly	Gln	Gln	Arg	Arg	Arg		
					130				135						140		
Ile	Thr	Ser	Val	Gln	Pro	Pro	Thr	Gly	Leu	Gln	Glu	Trp	Leu	Lys	Met		
					145				150						155		160
Phe	Gln	Ser	Trp	Ser	Gly	Pro	Glu	Lys	Leu	Leu	Ala	Leu	Asp	Glu	Leu		
					165				170						175		
Ile	Asp	Ser	Cys	Glu	Pro	Thr	Gln	Val	Lys	His	Met	Met	Gln	Val	Ile		
					180				185						190		
Glu	Pro	Gln	Phe	Gln	Arg	Asp	Phe	Ile	Ser	Leu	Leu	Pro	Lys	Glu	Leu		
					195				200						205		
Ala	Leu	Tyr	Val	Leu	Ser	Phe	Leu	Glu	Pro	Lys	Asp	Leu	Leu	Gln	Ala		
					210				215						220		
Ala	Gln	Thr	Cys	Arg	Tyr	Trp	Arg	Ile	Leu	Ala	Glu	Asp	Asn	Leu	Leu		
					225				230						235		240
Trp	Arg	Glu	Lys	Cys	Lys	Glu	Glu	Gly	Ile	Asp	Glu	Pro	Leu	His	Ile		
					245				250						255		
Lys	Arg	Arg	Lys	Val	Ile	Lys	Pro	Gly	Phe	Ile	His	Ser	Pro	Trp	Lys		
					260				265						270		

332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly
 275 280 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile
 290 295 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp
 305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr
 325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn
 340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala
 355 360 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val
 370 375 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp
 385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val
 405 410 415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg
 420 425 430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro
 435 440 445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val

450		455		460
Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp				
465		470		475 480
Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr				
	485		490	495
Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn				
	500		505	510
Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile				
	515		520	525
Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln				
	530		535	540
Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser				
545		550		555 560
Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe				
	565		570	575
Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val				
	580		585	590
Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser				
	595		600	605
Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val				
	610		615	620
Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu				
625		630		635 640

66659 66660

Ser Arg Gly Pro Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly
645 650 655

Leu Asp Ser Thr Arg Thr Gly His His His His His His
660 665

<210> 26

<211> 2001

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MYCHIS tagged
homo sapiens

<400> 26

atgtgtgtcc cgagaagcgg tttgatactg agctgcattt gcctttactg tggagttttg 60
ttgccgggttc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120
tctgtgacat acctacctga aaaaggttta tattgtcaga gactgccaaag cagccggaca 180
cacgggggca cagaatcact gaaggggaaa aatacagaaa atatggggtt ctacggcaca 240
ttaaaaatga ttttttacia aatgaaaaga aagttggacc atggttctga ggtccgctct 300
ttttctttgg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360
ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420
caacgacgcc gaattacatc tgtccagcca cctacagccc tccaggaatg gctaaaaatg 480
tttcagagct ggagtggacc agagaaattg cttgcttag atgaactcat tgatagttgt 540
gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac ccagtttca acgagacttc 600
atttcattgc tccctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660
ctgctacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720
tggagagaga aatgcaaaga agaggggatt gatgaaccat tgcacatcaa gagaagaaaa 780
gtaataaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840
attgatacta actggaggcg aggagaactc aaatctcta aggtgctgaa aggacatgat 900
gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960
aacactttaa aagtttggtc agcagtcaca ggcaaatgtc tgagaacatt agtgggacat 1020

685850 = 232220

123456789101112131415161718192021222324252627

acaggtggag tatggtcac acaaatgaga gacaacatca tcattagtgg atctacagat 1080
 cggacactca aagtgtggaa tgcagagact ggagaatgta tacacacctt atatgggcat 1140
 acttccactg tgcgttgtat gcatcttcat gaaaaaagag ttgttagcgg ttctcgagat 1200
 gccactotta gggtttggga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260
 gttgcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320
 tttatggtaa aggtgtggga tccagagact gaaacctgtc tacacacgtt gcaggggcat 1380
 actaatagag tctattcatt acagtttgat ggtatccatg tggtgagtgg atctcttgat 1440
 acatcaatcc gtgtttggga tgtggagaca ggggaattgca ttcacacgtt aacagggcac 1500
 cagtcgttaa caagtggaat ggaactcaa gacaatattc ttgtctctgg gaatgcagat 1560
 tctacagtta aaatctggga tatcaaaaca ggacagtgtt tacaacatt gcaaggctcc 1620
 aacaagcatc agagtgtgt gacctgttta cagttcaaca agaactttgt aattaccagc 1680
 tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740
 gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800
 aagctgggtg gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctggtgctg 1860
 gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920
 tctagagggc ccttogaaca aaaactcatc tcagaagagg atctgaatat gcataccggt 1980
 catcatcacc atcaccattg a 2001

<210> 27

<211> 666

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MYCHIS tagged
 homo sapiens

<400> 27

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr
 1 5 10 15
 Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr
 20 25 30
 Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

66650-23660

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu
225 230 235 240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile
245 250 255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys
260 265 270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly
275 280 285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile
290 295 300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp
305 310 315 320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr
325 330 335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn
340 345 350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala
355 360 365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val
370 375 380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp
385 390 395 400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val

000000000000000000000000

		405							410						415
Leu	Met	Gly	His	Val	Ala	Ala	Val	Arg	Cys	Val	Gln	Tyr	Asp	Gly	Arg
		420						425					430		
Arg	Val	Val	Ser	Gly	Ala	Tyr	Asp	Phe	Met	Val	Lys	Val	Trp	Asp	Pro
		435					440						445		
Glu	Thr	Glu	Thr	Cys	Leu	His	Thr	Leu	Gln	Gly	His	Thr	Asn	Arg	Val
		450				455						460			
Tyr	Ser	Leu	Gln	Phe	Asp	Gly	Ile	His	Val	Val	Ser	Gly	Ser	Leu	Asp
465					470						475				480
Thr	Ser	Ile	Arg	Val	Trp	Asp	Val	Glu	Thr	Gly	Asn	Cys	Ile	His	Thr
				485					490						495
Leu	Thr	Gly	His	Gln	Ser	Leu	Thr	Ser	Gly	Met	Glu	Leu	Lys	Asp	Asn
			500						505					510	
Ile	Leu	Val	Ser	Gly	Asn	Ala	Asp	Ser	Thr	Val	Lys	Ile	Trp	Asp	Ile
		515					520							525	
Lys	Thr	Gly	Gln	Cys	Leu	Gln	Thr	Leu	Gln	Gly	Pro	Asn	Lys	His	Gln
		530					535						540		
Ser	Ala	Val	Thr	Cys	Leu	Gln	Phe	Asn	Lys	Asn	Phe	Val	Ile	Thr	Ser
545					550						555				560
Ser	Asp	Asp	Gly	Thr	Val	Lys	Leu	Trp	Asp	Leu	Lys	Thr	Gly	Glu	Phe
				565						570					575
Ile	Arg	Asn	Leu	Val	Thr	Leu	Glu	Ser	Gly	Gly	Ser	Gly	Gly	Val	Val
			580						585						590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser
595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val
610 615 620

Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu
625 630 635 640

Ser Arg Gly Pro Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
645 650 655

Met His Thr Gly His His His His His His
660 665

*Sub
at
cont*

666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700